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1 **Identification and characterization of multiple porcine astrovirus genotypes**  
2 **in the Hunan province, China**

3

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26 **ABSTRACT**

27 Astroviruses (AstV) can infect a variety of hosts including mammalian and avian species and  
28 are commonly associated with enteric infections. Recently mammalian AstVs have been  
29 linked to extra-intestinal manifestations, including neurologic disorders in humans, cattle and  
30 minks, demonstrating a zoonotic potential. Until now, five porcine AstV (PAstV) genotypes  
31 have been identified, with PAstV1, PAstV2, PAstV3 and PAstV5 implicated in cross-species  
32 transmission. The knowledge on PAstV epidemiology in China is still limited. In this study,  
33 two duplex differential RT-PCRs were developed to investigate the distribution and  
34 prevalence of PAstV1, PAstV2, PAstV4 and PAstV5. Two-hundred-eighteen samples were  
35 collected from 33 farms and pigs with known diarrhea status in nine regions of the Hunan  
36 province in China. Specifically, 126 small intestines, 51 fecal swabs, 20 lungs, 19 spleens and  
37 two kidneys were obtained. PAstVs were detected in all nine regions and in 81.8% (27/33) of  
38 the investigated pig farms. The overall PAstV prevalence was 46.3% (101/218), with PAstV5  
39 as the predominant type with a positive rate of 24.8% (54/218). The prevalence of PAstV4,  
40 PAstV1 and PAstV2 was 16.1% (35/218), 14.7% (32/218) and 10.1% (22/218), respectively.  
41 Besides being present in intestines and fecal swabs, PAstV RNA was also detected in lungs,  
42 spleens and kidneys. Sequencing revealed a high genetic divergence within each genotype  
43 and a higher positive rate of PAstV5 was associated with pigs with diarrhea compared to pigs  
44 without diarrhea. This study discovered PAstV4 circulating in China for the first time, and  
45 revealed PAstV5 as the dominant genotype in pig herds in the Hunan province in China.

46 **Keywords:** Porcine astrovirus; Prevalence; Phylogenetic analysis; China; Pigs.

## 47 **Introduction**

48           Astroviruses (AstV), which belong to family *Astroviridae*, are small, non-enveloped,  
49 positive-sense single-stranded RNA viruses, with genomes of 6.4 to 7.7 kb in length, which  
50 are characterized by five- or six-pointed star-like surfaces [3]. Two genera have been defined,  
51 namely *Avastrovirus* infecting birds and *Mamastrovirus* infecting mammals [3]. Infection  
52 with *Avastrovirus* species often involves intestinal or extra-intestinal manifestations (e.g.  
53 damage to the liver, kidney, or the immune system) while infection with *Mamastrovirus* is  
54 predominantly associated with gastroenteritis [3]. Recently, member of the *Mamastrovirus*  
55 genus have been associated with extra-intestinal manifestations [7, 9, 20, 24, 25], including  
56 encephalitis in cattle [16, 26, 27] and a shaking syndrome in mink [1]. These findings may  
57 indicate that the clinical significance of AstVs in mammals is increasing.

58           Porcine astrovirus (PAstV) was first identified by electron microscopy in 1980 [4] and  
59 was isolated in 1990 [30]. Since then, PAstVs have been identified worldwide, including  
60 Africa, Asia, North America, and South America [10, 14, 33, 35]. Five genetically distinct  
61 genotypes (PAstV1 to PAstV5) have been defined with different prevalence and were  
62 identified in pig regardless of clinical signs [13, 28, 33]. It has been suggested that PAstV1,  
63 PAstV2, PAstV3 and PAstV5 may have crossed host species previously [21, 33]. In China,  
64 the knowledge for PAstV is still limited, with only four studies reporting the identification  
65 and distribution of PAstV. Specifically, a PAstV sequence belonging to PAstV2 (HQ647383)  
66 has been identified in domestic pigs with diarrhea in 2009 [12], a PAstV1 (GQ914773) strain  
67 was described in healthy domestic pigs in 2008 [29], and a PAstV2 (KP747573) sequence and  
68 a PAstV5 (KP747574) sequence were obtained from healthy domestic piglets [15]. Very

69 recently, several PAstV2 and PAstV5 sequences were identified in domestic pigs or wild  
70 boars in the Sichuan province, China [8]. However, generally, the PAstV genetic diversity  
71 and prevalence of different PAstV genotypes in China is still not well understood.

72 In the present study, we report the discovery of PAstV4 in China and the prevalence of  
73 PAstV1, PAstV2, PAstV4 and PAstV5 in domestic pigs from Hunan province, China.

74

## 75 **Materials and methods**

### 76 **Sample collection**

77 Two-hundred-and-eighteen independent samples were randomly collected from  
78 January to August of 2014 and included 126 small intestines, 51 fecal swabs, 20 lung tissues,  
79 19 spleens and two kidneys. The majority of the samples were from diagnostic case  
80 submissions to the College of Veterinary Medicine of Hunan Agricultural University.  
81 Samples were included based on availability at the time of sample collection resulting in  
82 limited numbers of lung, spleen and kidney samples compared to small intestines and fecal  
83 swabs. To avoid possible cross-contaminations, samples were collected with sterile  
84 instruments and whenever possible on different days. The samples came from 33 pig farms  
85 located in nine regions/cities of the Hunan province, China, including Changsha, Hengyang,  
86 Yiyang, Changde, Xiangtan, Chenzhou, Loudi, Zhuzhou and Yueyang. Among the samples,  
87 98 were from pigs with a history of diarrhea, and the remaining 120 samples were from pigs  
88 without clinical signs of diarrhea. The age of the pigs sampled ranged from 7 to 60 days. The  
89 samples were shipped on ice and kept in a -80 °C freezer until use.

90

### 91 **Sample processing and viral RNA extraction**

92           After re-suspending the fecal swabs in 1 ml sterile PBS, they were centrifuged at 4000  
93 rpm for 10 min, and 0.2 ml of the suspension was transferred into a 2 ml Eppendorf tube and  
94 used for viral RNA extraction. For tissue samples, approximately 0.1 gram of each the sample  
95 was placed into a 2 ml Eppendorf tube containing four 1.5 mm steel balls and were grinding  
96 using the Mixer Mill MM 400 (Retsch, Germany) for 1 min. Then 1 ml TRIzol reagent  
97 (Invitrogen<sup>TM</sup>) was added into the 2 ml tubes and RNA was extracted according to the  
98 manufacturer's instructions. The viral cDNA was synthesized by using the Transcriptor First  
99 Strand cDNA Synthesis Kit (Roche<sup>TM</sup>) and random primers as described by the manufacturer.  
100 The obtained viral cDNA were stored at -80 °C freezer.

101

#### 102 **Development of two duplex differential RT-PCR assays for detecting PAsTVs**

103           Based on the alignments of the available genome sequences of PAsTV, four pairs of  
104 primers were designed within conserved regions aiming to amplify PAsTV1 and PAsTV2 and  
105 PAsTV4 and PAsTV5 (Table 1). As the prevalence of PAsTV3 has been reported to be very low,  
106 only one genome of PAsTV3 (JX556691) is available in GenBank, and as the genetic  
107 heterogeneity within PAsTV genotypes is large [33], the prevalence of PAsTV3 was not  
108 investigated in the present study. Initially, single-plex RT-PCR assays were designed and  
109 tested and once optimized two duplex differential RT-PCRs with the same primer pairs  
110 targeting PAsTV1-2 and PAsTV4-5 were developed. The PCR assays were carried out in a 30  
111 µl total reaction volume containing 15 µl PCR mix (TIANGEN, Beijing, China), 0.5 µl of 10  
112 mM of each of the primers, 2 µl cDNA, and nuclease-free H<sub>2</sub>O. The amplification reactions  
113 were performed under the following conditions: 2 min at 94°C, 35 cycles of 30 s at 94°C, 20 s

114 at 57°C and 30 s at 72°C, followed by 72 °C for 7 min. The PCR products were then checked  
115 on a 0.8 % agarose gel under UV light, and the samples with positive results were recorded.

116 The sensitivity of the two duplex differential RT-PCR was evaluated by serial dilution  
117 of the cDNA used in the single-plex PCR. The specificity of the primers was confirmed by  
118 BLAST analysis, and in addition, positive controls for other swine RNA viruses including  
119 porcine transmissible gastroenteritis virus (TGEV), porcine reproductive and respiratory  
120 syndrome virus (PRRSV), porcine epidemic diarrhea virus (PEDV) and classical swine fever  
121 virus (CSFV) were tested with the two duplex differential RT-PCR assays.

122

### 123 **DNA sequencing and sequence analysis**

124 Four pairs of primers, located in open reading frame (ORF) 1b or ORF2, were  
125 designed to amplify the partial genome sequences of the four PAsV genotypes. The two pairs  
126 of primers used for PAsV1 and PAsV2 were the same as the single and duplex differential  
127 RT-PCR reactions ([Table 2](#)). The PCR products were checked under UV light, gel purified by  
128 QIAquick Gel Extraction Kit (QIAGEN Inc.), and the purified products were sequenced  
129 directly using the forward and reverse primers. The obtained sequences were analyzed by  
130 DNAMAN 7.0 (Lynnon Corporation) and the phylogenetic analysis was performed by the  
131 Neighbor-Joining method with the p-distance model through MEGA 6.0 [\[31\]](#).

132

### 133 ***Statistical analysis***

134 Differences in prevalence were investigated by chi-square tests using the JMP®  
135 Pro12.0.1 software (SAS, Cary, NC, USA). A *P* value less than 0.05 was considered

136 significant.

137

### 138 **GenBank accession numbers**

139 The nucleotide sequences obtained in the present study were deposited in GenBank  
140 under the following accession numbers: KY047664 - KY047762

141

## 142 **Results**

### 143 **Assay validation**

144 The sensitivity of the duplex differential RT-PCR assays was comparable to the  
145 single-plex RT-PCR assays, and the specificity of both duplex-RT-PCR assays and the four  
146 single-plex RT-PCR assays was 100% as viral RNA of TGEV, PRRSV, PEDV and CSFV  
147 was not detected (data not shown). Examples of the bands obtained with the two duplex  
148 differential RT-PCRs separated by agar gel electrophoreses are showed in Fig. 1.

149

### 150 **Prevalence of PAsTVs**

151 PAsTV was detected on 27 of the 33 (81.8%) farms investigated, and all of the nine  
152 regions in the Hunan province were positive, with an overall PAsTV positive rate of 46.3%  
153 (101/218) ([Table 3](#)). All of the four investigated PAsTV genotypes were discovered in the  
154 Hunan province, with PAsTV5 having the highest prevalence of 24.8% (54/218), followed by  
155 PAsTV4 with a prevalence of 16.1% (35/218). PAsTV1 and PAsTV2 showed low positive rates  
156 of 14.7% (32/218) and 10.1% (22/218), respectively.

157 When the PAsTV prevalence was compared in pigs with or without enteric signs, it was  
158 was 57.1% (56/98) in pigs with diarrhea compared to 37.5% (45/120) in pigs without diarrhea



159 which was significantly ( $P < 0.05$ ) different (Table 4). Furthermore, when genotype  
160 prevalence rates were compared, PAstV5 had a significantly ( $P < 0.05$ ) higher infection rate in  
161 pigs with enteric signs compared to pigs without diarrhea, while clinical status of a pig did not  
162 affect the prevalence of PAstV1, PAstV2 and PAstV4 (Table 4). The sample types with the  
163 highest infection rate were small intestines (52.4%) and fecal swabs (49%) (Table 5). PAstV  
164 was also detected in lungs, spleens and kidneys with a considerable high rate (Table 5), which  
165 may indicate that PAstVs could have a wide tissue tropism not limited to the intestine.  
166 However, due to the limited sample size for extra-enteric sample types, results need to be  
167 interpreted with caution and additional studies to further confirm the obtained results are  
168 needed. None of the lung tissues, spleen tissues and kidneys used in this study was obtained  
169 from pigs with a history of diarrhea.

170

### 171 **Molecular and phylogenetic analysis**

172 Sequencing was successful on 16 PAstV1 PCR products, 12 PAstV2 PCR products, 32  
173 PAstV4 PCR products and 39 PAstV5 PCR products, and the p-distances between the  
174 sequences within the same genotypes were calculated. For PAstV1, the obtained 16 sequences  
175 corresponded to five geographic regions/cities, with the identities between them ranging from  
176 90.4% to 100%. All showed a closer relationship to the GenBank PAstV1 sequence  
177 (KF787112) from the Guanxi province, China, with an average homology of 91.4%.  
178 Moreover, in the phylogenetic analysis, the present 16 PAstV1 sequences clustered into a  
179 single clade, and clustered together with PAstV1 (KF787112) from Guanxi province, China  
180 (Fig. 1). Based on the phylogenetic analysis, PAstV1 could be classified into two subclades,

181 PAstV1-1 and PAstV1-2, and the sequences obtained in this study clustered all within  
182 PAstV1-2. PAstV1-1 includes old PAstV1 sequences identified before 2008 from Japan,  
183 Canada and China. Moreover, from the present analysis, PAstV1 showed a close relationship  
184 with AstVs recovered from cats, California sea lions, and the classic human AstV (Fig. 2).

185 For PAstV2, the present 12 sequences corresponded to four different regions and  
186 showed identities of 98.2%-100% between each other, with an average of 82.1% identity to  
187 other available PAstV2 sequences in GenBank. Phylogenetic analysis indicated that the  
188 present PAstV2 sequences from the Hunan province clustered into a monophyletic group (Fig.  
189 3). Interestingly, AstV sequences recovered from porcupines (KJ571486) and roe deer  
190 (HM447046) clustered also with the PAstV2 group, possible indicating a recent cross-species  
191 transmission.

192 The 32 PAstV4 sequences were from seven regions of Hunan province with identities  
193 of 93.4% -100% between each other. In the phylogenetic analysis, the present sequences were  
194 clustered into two subgroups, designated as Hunan-1 and Hunan-2 groups (Fig. 4). The  
195 Hunan-1 group showed a close relationship with PAstV4 sequences from Spain, while the  
196 Hunan-2 group showed a closer relationship with some Italian PAstV4 strains (Fig. 4).  
197 PAstV4 sequences in GenBank have a global distribution and have been identified in Europe,  
198 Asia and North America (Fig. 4). Of note, except the PAstV4 sequences identified in the  
199 present study, no other PAstV4 sequence have been reported from China to date, although  
200 PAstV4 have high prevalence rates in other countries.

201 PAstV5 was detected in all of the nine investigated regions, with genetic identities of  
202 92.7% to 100% between each other, and an average identity of 97.5% within the genotype.

203 Moreover, PAstV5 from the Hunan province formed a monophyletic branch in the  
204 phylogenetic analysis, and showed a closer relationship to PAstV5 from US pigs than to a  
205 PAstV5 sequence (KP747574) previously identified in China (Fig. 5).

206

## 207 **Discussion**

208 The present PAstV overall positive rate of 46.3% (101/218) in domestic pigs from the  
209 Chinese Hunan province is much higher than the 17.5 % (21/120) reported recently from the  
210 Chinese Sichuan province [8], 19.4% (25/129) from South Korea [14], 20.8% (25/120) from  
211 Germany [18], and comparable to 34.2%, (67/196) from the Czech Republic [11], while it is  
212 lower than the prevalence rate of 79.2% (76/96) from Canada [17], 89% (81/91) from Croatia  
213 [6], 67.4%(163/242) from Italy [19], 100% from both Spain (83/83) and Australia (136/136)  
214 [35], 85.7% (36/42) from Hungary [35], and 64% (326/509) from the USA [33]. Moreover, in  
215 previous studies, PAstV2 or PAstV4 were reported to be the predominant genotypes in  
216 domestic pigs [6, 14, 17, 19, 33, 35], while in the present investigation, PAstV5 was firstly  
217 revealed to be the predominant genotype (24.8%,54/218) followed by PAstV4 (16.1%,  
218 35/218). This is also different compared to previous investigations in the Sichuan province,  
219 China, which indicated prevalence rates of 10% (12/120) for PAstV2 and 7.5% (9/120) for  
220 PAstV5 [8]. The different results may be due to differences in the efficacy of different  
221 primers used; moreover, PAstV has a large genetic divergence between genotypes but also  
222 within each genotype, which makes it is difficult to design universal primers (including  
223 degenerate primers) suitable for all know or unknown PAstV strains. On the other hand, the  
224 distribution and prevalence of PAstV genotypes may be different among regions or countries.

225 Under experimental conditions using caesarian-derived, colostrum-deprived 4-day-old  
226 pigs, PAstV1 infection could be associated with mild diarrhea [30]. However, any association  
227 of the other four PAstV genotypes with clinic manifestations in pigs remains undetermined. It  
228 has been reported that diarrheic pigs had a higher viral load of PAstV4 in nursery and  
229 growing-finishing groups [35]. In the present study, PAstVs and more specifically PAstV5  
230 had a significantly higher prevalence in pigs with diarrhea compared to pigs without diarrhea.  
231 This is in contrast to most other studies which reported no significant association of PAstV  
232 infection and diarrhea [5, 17, 19, 28]. Further virus isolation and pathogenicity studies are  
233 needed to clarify the importance of this group of viruses in pigs.

234 Many mammalian AstV have been detected in extra-enteric tissues. Murine AstVs has  
235 been detected in the spleen, liver, kidney and mesenteric lymph nodes [22, 34]. Novel bovine  
236 and mink AstVs have been discovered in brain tissues [1, 16, 32], and novel human AstVs  
237 have been discovered in brain tissues, serum samples, cerebrospinal fluid and urine [24, 25].  
238 PAstV RNA could be detected in the blood of healthy pigs [5] and in nasal swabs from pigs  
239 with acute respiratory symptoms [23]. In the present study, PAstV has been detected in spleen,  
240 lung and kidney tissues. However, due to the limited number of extra-enteric samples  
241 available for this study the obtained results require confirmation in additional studies which  
242 should include larger numbers of pigs and a defined standard set of samples from each pig.  
243 Nevertheless, these data further confirm that mammalian AstV have a wide tissue tropism and  
244 are not restricted to enteric tissues. A potential role of PAstV in extra-enteric diseases  
245 including neurologic disorder has been suggested previously [2].

246 In conclusion, the present study demonstrates the presence of PAstV1, PAstV2,

247 PAstV4 and PAstV5 in domestic pigs located in the Hunan province, China. To our  
248 knowledge, this is the first description of PAstV4 in Chinese pigs. Furthermore, the PAstV  
249 genotype distribution in China appears to be substantially different compared to other  
250 geographic regions with a high prevalence of PAstV5 in domestic pig herds instead of  
251 PAstV2 or PAstV4. Within the PAstV genotypes from the Hunan province a high genetic  
252 diversity has also been revealed.

253

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259

### 260 **Conflict of interest**

261 The authors declare that they have no conflict of interest.

262

### 263 **Compliance with Ethical Standards**

264 The experiments were approved and carried out in accordance with animal ethics guidelines  
265 and approved protocols of the Hunan Agricultural University.

266

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268

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381 **Table 1.** Primer information for porcine astrovirus (PAstV) detecting single or duplex RT-PCR assays.

382

Genotype	Primer	Sequence (5' →3')	Position	Reference sequence	Size
PAstV1	AV1-F	5`-TCCTGTGCTATCAGTTGCTCTC-3`	4032-4053	GQ914773	420
	AV1-R	5`-GATTGCTGGTTTTGGACCTGTG-3`	4430-4451		
PAstV2	AV2-F	5`-AGCAGCTGGATCGTCTTTGGA-3`	3933-3953	JX556690	827
	AV2-R	5`-AGATTCAGCATCCCAGGTTGTT-3`	4738-4759		
PAstV4	AV4-F	5`-TGGCTTCAGGCCTTTGAGTTTT-3`	3588-3609	JX556692	559
	AV4-R	5`-CACCGTCGTAGTAGTCGTGAC-3`	4126-4146		
PAstV5	AV5-F	5`-TGGTACGTRCACAATCTGTTGAA-3`	3562-3584	JX556693	182
	AV5-R	5`-TCAGTGTCTTCCCAACCRTC-3`	3724-3743		

383

384 **Table 2.** Primers used to sequence porcine astroviruses (PAstV).

385

Genotype	Sequence (5' →3')	Location	Position	Reference sequence	Expected size
PAstV4	F:GTCTATGGRGACGACAGATTGAC	ORF 1b	3660-3682	JX556692	425 bp
	R:TTATGCTTTGGTCCGCCCTC	ORF 1b	4064-4084		
PAstV5	F:ACCAACTTCCCTCCCGACCC	ORF 1b	3778-3797	JX556693	368 bp
	R:TACGACAAGATCCTATCTGAAAAG	ORF2	4122-4145		

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389 **Table 3.** Porcine astrovirus (PAstV) genotypes detected in different regions/cities of the  
 390 Hunan province, China.

391

Regions	PAstV1	PAstV2	PAstV4	PAstV5	Co-infection	Overall
Changde	1/6 (16.6%)	0/6 (0%)	0/6 (0%)	2/6 (33.3%)	1/6 (16.6%)	2/6 (33.3%)
Changsha	8/85 (9.4%)	12/85 (14.1%)	21/85 (24.7%)	23/85 (27.1%)	18/85(21.2%)	46/85 (54.1%)
Xiangtan	4/22 (18.2%)	0/22 (0%)	4/22 (18.2%)	7/22 (31.8%)	5/22(22.7%)	10/22 (45.5%)
Chenzhou	2/19 (10.5%)	1/19 (5.3%)	2/19 (10.5%)	5/19 (26.3%)	2/19 (10.5%)	8/19 (42.1%)
Hengyang	8/39 (20.5%)	3/39 (7.7%)	4/39 (10.3%)	6/39 (15.4%)	8/39 (20.5%)	13/39 (33.3%)
Loudi	0/4 (0%)	1/4 (25%)	0/4 (0%)	2/4 (50%)	0/4 (0%)	3/4(75%)
Zhuzhou	3/15 (13.3%)	3/15 (20%)	1/15 (6.7%)	2/15 (13.3%)	3/15 (13.3%)	6/16 (40%)
Yiyang	2/16 (12.5%)	2/16 (12.5%)	1/16 (6.3%)	3/16 (18.7%)	4/16 (25%)	4/16 (25%)
Yueyang	4/12 (33.3%)	0/12 (0%)	2/12 (16.7%)	4/12 (33.3%)	1/12(8.3%)	9/12 (75%)
Total	32/218 (14.7%)	22/218 (10.1%)	35/218 (16.1%)	54/218 (24.8%)	42/218(19.3%)	101/218 (46.3%)

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394

395 **Table 4.** Porcine astrovirus (PAstV) infection rate by genotype in pigs with a history of  
 396 diarrhea or without diarrhea.

Disease Status	PAstV1	PAstV2	PAstV4	PAstV5	Overall
No diarrhea	15.8% (19/120)	11.7% (14/120)	14.2% ( 17/120)	20% (24/120)	37.5% (45/120)
Diarrhea	12.2% (12/98)	8.2% (8/98)	18.4% (18/98)	31.6% (31/98)	57.1% (56/98)

397

398

399 **Table 5.** Infection rate of different porcine astroviruses (PAstV) genotypes in selected samples  
 400 types.

401

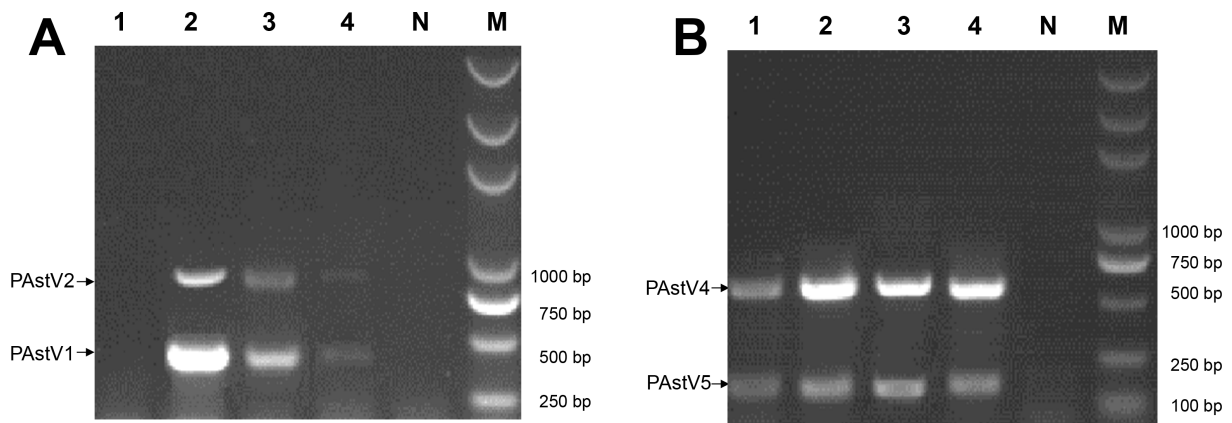
Sample type	PAstV1	PAstV2	PAstV4	PAstV5	Overall
Small intestine	12.7% (16/126)	9.5% (12/126)	15.9% (20/126)	29.4% (37/126)	52.4% (66/126)
Fecal swab	17.6% (9/51)	7.8% (4/51)	25.5% (13/51)	27.5% (14/51)	49% (25/51)
Spleen	5.3% (1/19)	10.5% (2/19)	5.3% (1/19)	15.8% (3/19)	15.8% (3/19)
Lung	20% (4/20)	20% (4/20)	0% (0/20)	5% (1/20)	25% (5/20)
Kidney	50% (1/2)	50% (1/2)	50% (1/2)	0%	100% (2/2)

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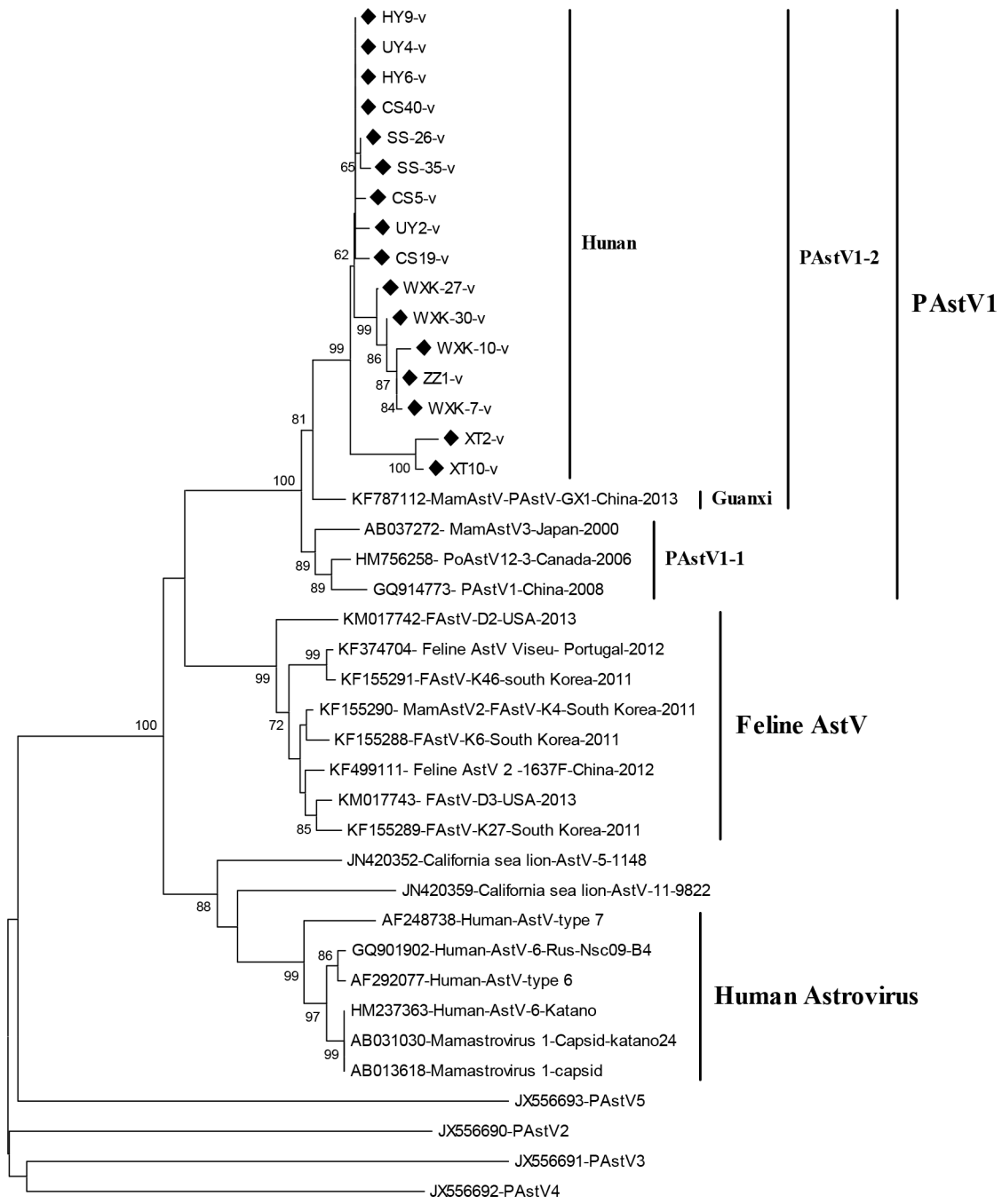
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405 **Figure legends**



406

407 **Fig.1** Gel-based electrophoresis of several selected samples to demonstrate the duplex  
408 differential RT-PCR outcome. The PCR products were separated on a 0.8 % agarose gel. (A)  
409 Duplex differential RT-PCR for PAstV1 (420bp) and PAstV2 (827bp). Lanes 1-4, selected  
410 clinic samples, lane 1 (negative), lanes 2-4 (positive for both PAstV1 and PAstV2); N,  
411 negative control; M, DNA molecular marker. (B) Duplex differential RT-PCR for PAstV4  
412 (559bp) and PAstV5 (182bp). Lanes 1-4, selected clinical samples, positive for both PAstV4  
413 and PAstV5; N, negative control; M, DNA molecular marker.

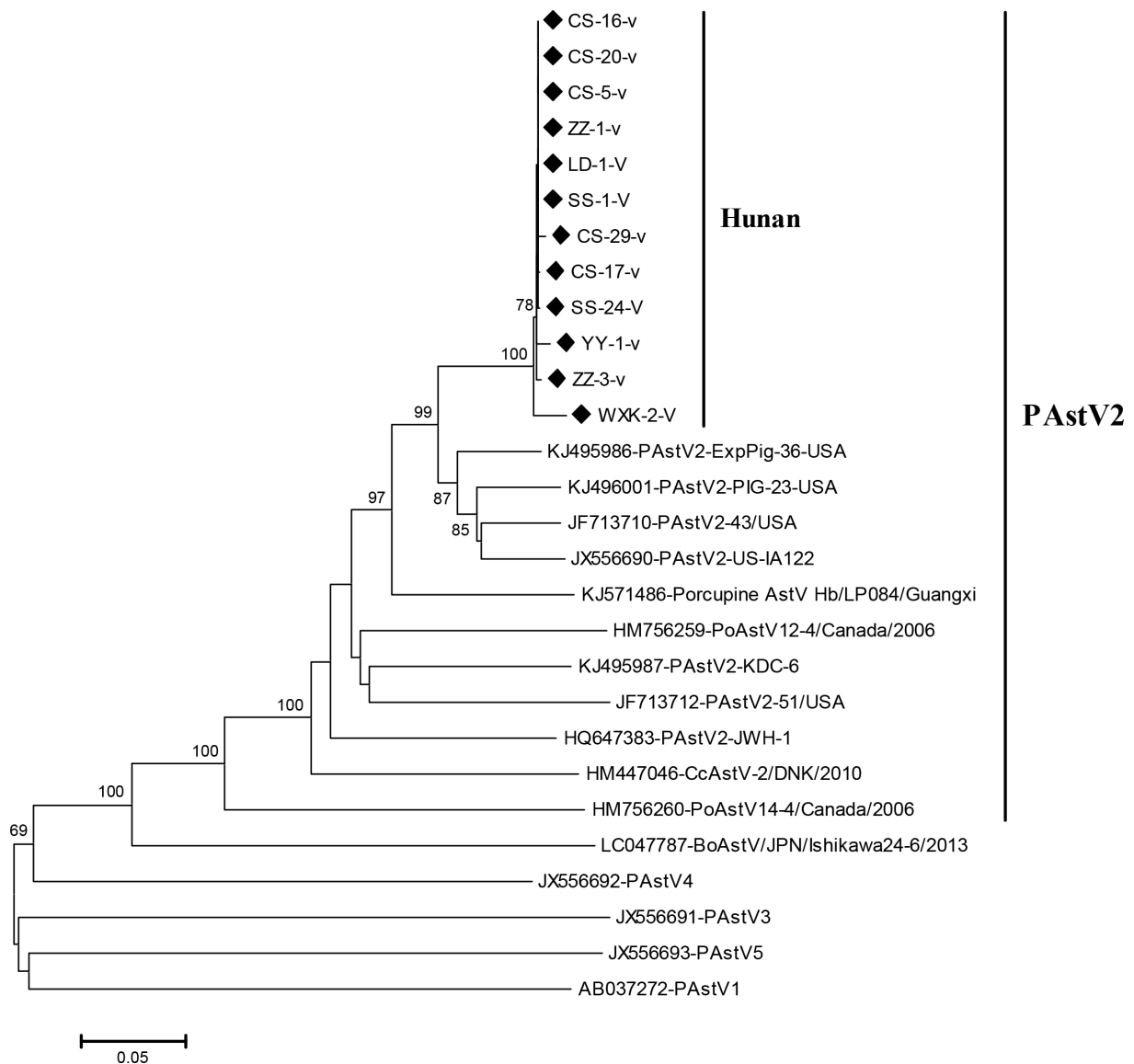


414



415 **Fig. 2** Phylogenetic analysis of PAsTV1 based on the 16 sequences identified in the present  
 416 study and 20 additional PAsTV1 sequences obtained through GenBank. The reference  
 417 sequences of PAsTV2 to PAsTV5 were included for comparison. The evolutionary tree was  
 418 inferred using the Neighbor-Joining method with the p-distance model. The percentage of  
 419 replicate trees in which the associated sequences clustered together in the bootstrap test (1000

420 replicates) are shown next to the branches (only >60% was shown). The tree is drawn to scale,  
 421 with branch lengths in the same units as those of the evolutionary distances used to infer the  
 422 phylogenetic tree. All positions containing gaps and missing data were eliminated. There were  
 423 a total of 304 positions in the final dataset. The PASTV1 strains identified presently were  
 424 indicated with black diamonds. The evolutionary analyses were conducted in MEGA6.



425  
 426 **Fig. 3** Phylogenetic analysis of PASTV2 based on the 12 sequences identified in the present  
 427 study and nine additional PASTV2 sequences obtained through GenBank. The reference  
 428 sequences of PASTV1, PASTV3, PASTV4, PASTV5 and AstV sequences obtained from porcupine,



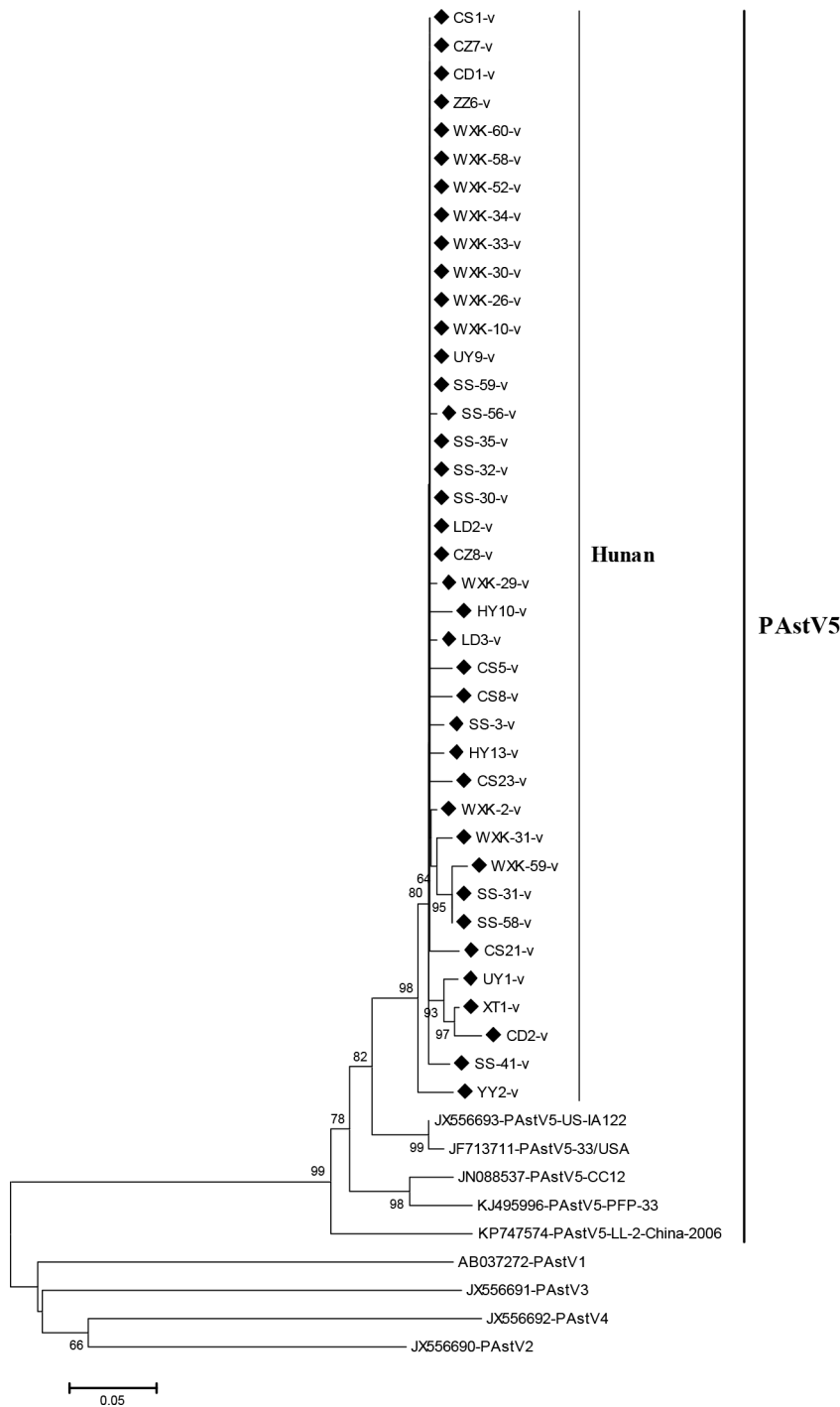
429 roe deer, and cattle were included for comparison. The evolutionary tree was inferred using  
430 the Neighbor-Joining method with the p-distance model. The percentage of replicate trees in  
431 which the associated sequences clustered together in the bootstrap test (1000 replicates) are  
432 shown next to the branches (only >60% was shown). The tree is drawn to scale, with branch  
433 lengths in the same units as those of the evolutionary distances used to infer the phylogenetic  
434 tree. All positions containing gaps and missing data were eliminated. There were a total of  
435 748 positions in the final dataset. The PAsV2 strains identified presently are indicated by  
436 black diamonds. The evolutionary analyses were conducted in MEGA6.



437

438 **Fig. 4** Phylogenetic analysis of PAsTV4 based on the 32 PAsTV4 sequences obtained in the

439 present study and 61 PAsV4 sequences available through GenBank. The reference sequences  
440 of PAsV1, PAsV2, PAsV3 and PAsV5 were included for comparison. The evolutionary tree  
441 was inferred using the Neighbor-Joining method with the p-distance model. The percentage of  
442 replicate trees in which the associated sequences clustered together in the bootstrap test (1000  
443 replicates) are shown next to the branches (only >60% was shown). The tree is drawn to scale,  
444 with branch lengths in the same units as those of the evolutionary distances used to infer the  
445 phylogenetic tree. All positions containing gaps and missing data were eliminated. There were  
446 a total of 189 positions in the final dataset. The PAsV4 strains identified in the present study  
447 are indicated by black diamonds. The evolutionary analyses were conducted in MEGA6.



448

449 **Fig. 5** Phylogenetic analysis of PASTV5 based on the 39 PASTV5 sequences identified in the  
 450 present study and five PASTV5 sequences available through GenBank. The reference  
 451 sequences of PASTV1, PASTV2, PASTV3 and PASTV4 were included for comparison. The  
 452 evolutionary tree was inferred using the Neighbor-Joining method with the p-distance model.  
 453 The percentage of replicate trees in which the associated sequences clustered together in the

454 bootstrap test (1000 replicates) are shown next to the branches (only >60% was shown). The  
455 tree is drawn to scale, with branch lengths in the same units as those of the evolutionary  
456 distances used to infer the phylogenetic tree. All positions containing gaps and missing data  
457 were eliminated. There were a total of 229 positions in the final dataset. The PAsV5 strains  
458 identified in the present study are indicated with black diamonds. The evolutionary analyses  
459 were conducted in MEGA6.